

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/552,013  
Source: PG/10  
Date Processed by STIC: 10/18/05

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PCT

## RAW SEQUENCE LISTING

DATE: 10/18/2005

PATENT APPLICATION: US/10/552,013

TIME: 10:16:52

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\10182005\J552013.raw

```

3 <110> APPLICANT: Renz, Andreas
4      Sozer, Nursen
5      Frentzen, Margit
6      Bauer, Jorg
7      Keith, Stobart
8      Fraser, Thomas
9      Lazarus, Colin M
10     Qi, Baoxiu
11     Abbadi, Amine
12     Heinz, Ernst
14 <120> TITLE OF INVENTION: NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED,
MULTIPLY
15     UNSATURATED FATTY ACIDS
17 <130> FILE REFERENCE: 13478-00002-US
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/552,013
C--> 19 <141> CURRENT FILING DATE: 2005-09-30
19 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/003224
20 <151> PRIOR FILING DATE: 2004-03-26
22 <150> PRIOR APPLICATION NUMBER: DE103 14 759.4
23 <151> PRIOR FILING DATE: 2003-03-31
25 <150> PRIOR APPLICATION NUMBER: DE103 48 996.7
26 <151> PRIOR FILING DATE: 2003-10-17
28 <160> NUMBER OF SEQ ID NOS: 122
30 <170> SOFTWARE: PatentIn version 3.3
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1047
34 <212> TYPE: DNA
35 <213> ORGANISM: Thraustochytrium
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (38)..(952)
40 <223> OTHER INFORMATION: LPAAT
42 <400> SEQUENCE: 1
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45                                     Met Ser Ala Trp Thr Arg
46                                     1           5
47 gcc aag acc gcc gtg ggc ctc ctg acg ctg gcg cct gcg cgg ata gtg      103
48 Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
49           10           15           20
50 ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc      151
51 Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
52           25           30           35
53 acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc      199
54 Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys

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55	40	45	50	
56	gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc	247		
57	Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val			
58	55 60 65 70			
59	tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg	295		
60	Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala			
61	75 80 85			
62	aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac	343		
63	Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His			
64	90 95 100			
65	tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc	391		
66	Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val			
67	105 110 115			
68	ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc	439		
69	Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly			
70	120 125 130			
71	ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct	487		
72	Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro			
73	135 140 145 150			
74	cct cga gat tcg tcg agc gag aag cac cac gcg cag ccg ctt ctt gtg	535		
75	Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val			
76	155 160 165			
77	ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag	583		
78	Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys			
79	170 175 180			
80	acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag	631		
81	Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu			
82	185 190 195			
83	ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg	679		
84	Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser			
85	200 205 210			
86	gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac	727		
87	Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His			
88	215 220 225 230			
89	cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag	775		
90	Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu			
91	235 240 245			
92	aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg	823		
93	Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala			
94	250 255 260			
95	cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc	871		
96	Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu			
97	265 270 275			
98	gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga	919		
99	Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly			
100	280 285 290			
101	gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca	972		
102	Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu			
103	295 300 305			

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104 agcgggtccag caacgggaga ttaaacacg atttcttagc ctacaaaaaa aaaaaaaaaa 1032
105 aaaaaaaaaa aaaaaa 1047
108 <210> SEQ ID NO: 2
110 <211> LENGTH: 305
111 <212> TYPE: PRT
113 <213> ORGANISM: Thraustochytrium
115 <400> SEQUENCE: 2
117 Met Ser Ala Trp Thr Arg Ala Lys Thr Ala Val Gly Leu Leu Thr Leu
118 1 5 10 15
119 Ala Pro Ala Arg Ile Val Phe Leu Val Thr Val Leu Gly Thr Tyr Gly
120 20 25 30
121 Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
122 35 40 45
123 Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
124 50 55 60
125 Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
126 65 70 75 80
127 Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
128 85 90 95
129 Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
130 100 105 110
131 Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
132 115 120 125
133 Ile Val Asp Arg Glu Gly Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
134 130 135 140
135 Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
136 145 150 155 160
137 Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
138 165 170 175
139 Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
140 180 185 190
141 Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
142 195 200 205
143 Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
144 210 215 220
145 Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
146 225 230 235 240
147 Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
148 245 250 255
149 Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
150 260 265 270
151 Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
152 275 280 285
153 Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
154 290 295 300
155 Leu
156 305
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 1701

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162 <212> TYPE: DNA
164 <213> ORGANISM: Physcomitrella patens
166 <220> FEATURE:
167 <221> NAME/KEY: misc_feature
168 <223> OTHER INFORMATION: LPAAT
170 <400> SEQUENCE: 3
172 ggcacgaggg aaattggctt tctatgtggc cgtacttatt cgaggaggtc aacgaaacaa      60
173 aggtatgtct tattaatgaa aatgtctcca cacatgtatg ttgttttaggt atattctgtc      120
174 aactgaaaac ttgttttaaat tttttcttaa attgaaattc tgtgcctgaa agccaactct      180
175 aggtccatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgct      240
176 tttgcaatth tcttttgctg ttaacctatt gattatgttg gaaccacaat acagacgctg      300
177 cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggttaatth catcctacag      360
178 ggatatggat gttgtaaagg tgatttttgc aggtgataaa gtacctaaagg agaaccgtgt      420
179 gatggcatg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat      480
180 tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc      540
181 cttgtttggt tgggcattth acgtttttga gtttctgatg ctgcatagaa agtgggaagt      600
182 ggatgctccc gtcatcaaga catacattga cagttttcaa gataaaagag atcctctctg      660
183 gctagtcgtg tttcctgaag gcacagattt ttcgtaaggc tgaagtacc atccatggct      720
184 ttgatgtata tctgcaatct tctctataat ctgcatttat tctctgttg tctctagca      780
185 agtaaatcat acttgcttaa tgtacttagc aatttgtcat ttttgactta ttgtgatgta      840
186 aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga      900
187 gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcactcgtgg ctttgtgact      960
188 tgcttttctc aatcgcgctg ctctttggat gcagtttatg acctcactat aggggtacaag     1020
189 aagcgggtgc cttgtttcat caacaatgta ttcggaaccg atccatcgga agtgcacatt     1080
190 cacattcgcc gaataccaat ttctgagatt cctcaatcag aagacgggat gacgcagtgg     1140
191 ctgtatgatc tattttatca aaaggaccag atgttggcca gttttagtaa gacaggctct     1200
192 ttccttgaca gtggaattga agagagccct ttgaacatag tgggaagggtg ttgcaatggt     1260
193 gctctacacg tagtccttag cggttgggta ttctgggtgct tgtttcattc ggtttgggtg     1320
194 aagctttatg tggttttcgc tagtttgctg ctgcggttta gtacctatth tgattggaga     1380
195 cctaaaccgg tttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcggt     1440
196 agttgtaatt ggtttgthta ttccgattcc aaagctgagt ttaagggtga ggctcctctt     1500
197 taagctgatt tttgctatta attggctgct cccttgthtg tctgocgtaa attggcttht     1560
198 atacggthgt cttctgctga tgaacctcag tgcttcaaga cgatgtggcc ttttagcctt     1620
199 ctcttttacc catcttgacc agatgccaac ctgcgaataa agcagatcaa taggtcgtgc     1680
200 cccaaaaaaaa aaaaaaaaaa a
203 <210> SEQ ID NO: 4
205 <211> LENGTH: 714
206 <212> TYPE: DNA
208 <213> ORGANISM: Physcomitrella patens
210 <220> FEATURE:
211 <221> NAME/KEY: CDS
212 <222> LOCATION: (1)..(714)
213 <223> OTHER INFORMATION: LPAAT
215 <400> SEQUENCE: 4
217 atg gct ttg atg tat atc tgc aat ctt ctc tat aat ctg cat tta ttc      48
218 Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
219 1 5 10 15
220 tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc      96
221 Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser

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222          20          25          30
223 aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat      144
224 Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
225          35          40          45
226 gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa      192
227 Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
228          50          55          60
229 ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt      240
230 Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
231 65          70          75          80
232 gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac      288
233 Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
234          85          90          95
235 ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta      336
236 Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
237          100          105          110
238 ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca      384
239 Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
240          115          120          125
241 att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat      432
242 Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
243          130          135          140
244 gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca      480
245 Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
246 145          150          155          160
247 ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg      528
248 Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
249          165          170          175
250 gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta      576
251 Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
252          180          185          190
253 ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc      624
254 Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
255          195          200          205
256 gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa      672
257 Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
258          210          215          220
259 ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtg taa      714
260 Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
261 225          230          235
263 <210> SEQ ID NO: 5
265 <211> LENGTH: 237
267 <212> TYPE: PRT
269 <213> ORGANISM: Physcomitrella patens
271 <400> SEQUENCE: 5
274 Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
275 1          5          10          15
276 Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
277          20          25          30

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**VERIFICATION SUMMARY**

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L:19 M:270 C: Current Application Number differs, Replaced Current Application No

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date